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FIGURE 1

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGA
 GAGAAGCGCTGCAGCCAACAGGGGTGAGGCTGTGCTCACAGTTTCTCTGGCGGCATGTAA
 AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC
 CAAGCCTTGAGACTGCGCAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAGA
 AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCT
 CTGTGGAGGCAGAGCCAGTGGAGCCCACTGAGGCAGGGCTGCTTGGCAGGCCACCGGCTGCA
 ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCGCTGACGGCCAGGGTGAAGCATG
 TGAGGAGCCGCCCGGAGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGA
 ATAACCACCATTTCGCAAGGACCATGAGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG
 CTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTGTAGGGCACTGAGGAGGGCTC
 GCCAAGAGAGTTTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCA
 CCTACACCTTCATTGTGCCCAAGCAGCGGGTACGGGTGCCATCTGCGTCAACTCCAAGGAG
 CCTGAGGTGCTTCTGGAGAACCAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCT
 GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG
 TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACCTGCGGGGTACGCGAGCTC
 TACATGCAAGCTCCTGCACGAGATCATCCGCAAGCGGGACACGCGTTGGAGCTCTCCAGCT
 GGAGAACAGGATCTCGAACACAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC
 TGGAGCACAAGTACAGCACTGGCCACACTGGCCACAACCAATCAGAGATCATCGCGCTC
 CTTGAGGAGCACTGCCAGAGGGTGGCCCTCGGCCAGGCGCCGTCCCCAGCCACCCCCGCTGC
 CCGCGCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG
 AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCCACTATGCCCACTCTC
 ACCAGCCTCCCATCTTCCACCGACAAGCCGTGCGGGCCATGGAGAGACTGCCTGCAGGCCCT
 GGAGGATGGCCACGACCAAGCTCCATCTACCTGGTGAAGCGGGAGAACACCAACCGCGTCA
 TGCAGGTGTGGTGCAGACCAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCGTG
 GATGGCTCTGTTAACTTCTTCAGGAACCTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGA
 CGGCAATACTGGCTGGGCTGGAGAACATTACTGGCTGACGAACCAAGGCAACTACAAC
 CTCTGGTGACCATGGAGGACTGGTCCGGCCGCAAGTCTTTGCAGAATACGCCAGTTTCCGC
 TGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA
 CTCCTTTACATGGCACAACGGCAAGCAGTTACCACCCTGGACAGAGATCATGATGTCTACA
 CAGGAACCTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCCTGTGCCCACTCCAAC
 CTCAACGGGGTCTGGTACCGCGGGGGCCATTACCAGGAGCGCTACCAGGACGGAGTCTACTG
 GGCTGAGTTCCGAGGAGGCTCTTACTACTCAAGAAAGTGGTGATGATGATCCGACCGAACCC
 CCAACACCTTCCACTTAAGCCAGCTCCCCCTCGACCTCTCGTGGCCATTGCCAGGAGCCCA
 CCTGGTCAGCTGGCCACAGCACAAAGAACAACCTCTCACCAGTTCATCCTGAGGCTGGGA
 GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAACCTGAATCAGT
 ACGGTGTTTTCTGTCCCTCTACTTTTCCTTCAACCAAGACAGCCCTCATGTCTCCAGGACA
 GGACAGGACTACAGACAACCTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

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FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRVTGAICVNSKEPEVLLNVRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLR
KESRNMNSRVLTOLYMQLLHEIIRKRDNALELSQLENRILNQATADMLQLASKYKDLCHKYQHL
ATLAHNQSEIIAQLEEHCRVPSARPVQPQPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSIIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFRRNWETKQGFNGIDGEYWLGLENIYWLTNQGNKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYHQ
KGGWWYNACAHNSNLNGVWYRGGHYRSRYQDGVYWAEEFRGGSYSLKKVVMIRPNPNTFH
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Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,
465-471, 473-479**Amidation site.**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

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FIGURE 3

CCCACGCGTCCGGCGCGGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCGCGCCGCCCTCCCTCCGGTGGGCGCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGAGTGGG
GCCGGGTAGGCTCTGGAAGGGCCCGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCAGGCGCCGCGCTTGAGGGATCTGAAGAGGTTCC TAGAAGAGGGT
GTTCCCTCTTTCGGGGTCTCTACCCAGAAGAGGTTCTTGGGGTTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAAATCCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTCACTTGTAAAAACAAATAGGATGCAAAATCC
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACACCTAAATGATCGTCTTTG
GTTGGGCGGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCGGCCACCAAGGAGGGC
CGAGGACCTCATGAGCCAAGGAGAAAAGAAACAAAATGTGGATGGCTAGTGTTGGACACACT
GGCAGTAATACGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAAT
GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

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FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846

<subunit 1 of 1, 117 aa, 1 stop

<MW: 12692, pI: 7.50, NX(S/T): 0

MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRRGRGPHEPRRKKQNV DGLVLDTLAVIRTLVDK

Important features:**Signal peptide:**

amino acids 1-16

N-myristoylation sites.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGGATCCCGG
CCCCGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGGGAGAA
GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAAGAGGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAAAACAAACAGG
CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSLEFTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLGHNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

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FIGURE 7

ATGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACACAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACAT**AG**

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FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIIVTRLYCRQGYLQMHPDGAIDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTEPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGHNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSITT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

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FIGURE 9

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCGCTGGCA
GACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAAGCT
GTGTCCAGACTGAGGCCCCATTTCGATTGTTTAAACATACTTAGAAAATGAAGTGTTCATTTT
TAACATTCCCTCCAATTGGTTTAATGCTGAATTACTGAAGAGGGCTAAGCAAAACAGGT
GCTTGCCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGCGCTCTCCCGTGTCTCTCCCA
CGACTCGCTCGGCCCTCTGGAATAAAACACCCGAGCCCGAGGGCCGAGGAGGGCCGGA
CGTGCCCGAGCTCTCTCGGGGGTCCCGCCCGCGAGCTTTCTTCTCGCCTTCGCACTCTCTCTCC
TCGCGCGTCTTGGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATCTGGGCTCTCTG
TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT
CAGGACAGTGTATAGATAATTGATGAATGCCGAACCATCCCCGAGGCGCTGCCGAGGAGACATG
ATGTGTGTTAACCAAAAATGGCGGGTATTTATGCATTCCCGGACAAACCCCTGTGTATCGAGG
GCCCTACTCGAACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCAC
TCTCAGCTCCAACATATCCCAAGATCTCCAGGCTCTTATATGCCGCTTTGGATACCAAGATG
GATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCACCCC
CACCAGATCTGCATCAATACTGAAGCGGGGTACACCTGCTCCTGCACCCAGCGATATTGGC
TTCTGGAAGGCGCATGCTGTAGACATTGATGAATGTGCGTATGGTTACTGCCAGCAGCTCTGT
GCGAATGTTCTCGATCTCTATTCTGTACATGCAACCCTGGTTTTACCTCAATAGGATGG
AAGTCTTCCCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGGCTGCGTGAACACTGTCTCA
ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAACCTTGAGGAAGATGGCGTT
CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCCTTGCCAACATGAGTGTGTGAA
CCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCTGCTGGATGACAACCGAA
GCTGCCAAGACATCAACGAATGTGAGCACAGGAACACACATGCAACCTCGACGAGACGTGC
TACAATTTACAAGGGGCTTCAATGCACTCGACCCCATCCGCTGTGAGGAGCCCTTATCTGAG
GATCAGTGATAACCGCTGTATGTGTCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTA
CCATCTTGTACCGGGACATGGACGTGGTGTGACGAGCTCCGTTCCCGCTGACATCTTCCAA
ATGCAAGCCACGACCCGCTACCTTGGGGCCTATTACATTTTCCAGATCAAACTCTGGGAATGA
GGCGAGAGAATTTTACATCGGGCAAACGGGCCCCATCAGTGCCACCTGGTGATGACACGCC
CCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGGAAATGATCACTGTCAACACTGTCTATC
AATTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTGCGCAGTACCCATTCTGAGC
CTCGGGCTGGAGCTCCGACGCTGCCTCTCATTTGGCACCAGGGGACAGGAGAAGAGAGGAAA
TAACAGAGAGAATGAGAGCGACACAGACGTTAGGCAATTTCTGTGAACCTTTCCCCGAAGA
CTCAGCCCCGACTTCTGACTCTCACCTGTACTATTGCAGACCTGTACCTTGCAGGACTTG
CCACCCCACTTCTATGACACAGTTATCAAAAGTATTATCATTTGCTCCCTGATAGAAGA
TTGTTGGTGAATTTCAAGGCCCTTCAGTTTATTTCCACTATTTTCAAGAAAATAGATTAGG
TTTGCGGGGTCTGAGTCTATGTTCAAAAGACTGTGAACAGCTTGCTGTCACTTCTTCACCTC
TTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCAAAGACCCGGGAGCTGGCGGGGAACCTT
GGGAGTAGCTAGTTTGCTTTTTGCGGTACACAGAGAAGGCTATGTAACAACAACCACAGCAGGA
TCGAAGGGTTTTAGAGAATGTGTTTCAAACCATGCCTGGTATTTTCAACCAATAAAGAAAG
TTTCAGTTGTCCTTAAATTTGATAACGGTTTAAATCTGCTTGTTCATTTTGTAGATTATTTT
AAAAAATATGTCGTAGAATTCCTTCGAAAGGCCCTTCAGACACATGCTATGTTCTGTCTTCCC
AAACCCAGTCTCCTCTCATTTTTCAGCCAGTGTTTTCTTGGAGGACCCCTTAATCTTGTCTT
CTTTAGAATTTTTACCAATTGGATTGGAATGCAGAGGTCTCCAACTGATTAATAATTTGA
AGAGA

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FIGURE 10

MPGIKRLTIVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ
 NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDENQ
 CVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQLCANVPG
 SYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSILICRCDPGYELEDGVHCSDM
 DECSFSEFLCQHECVNPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG
 GFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRVPADIFQMATT
 RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGS
 SVIRLRIYVSQYPF

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
 267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

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FIGURE 11

CAGGTCCAAC TGACCTCGGTTCTATCGATTGAAT TCCCCGGGGATCCTCTAGAGATCCCTC
 GACCTCGACCCACCGCTCCGAACACAGGTCCTTGTTGCTGCGAGAGAGCAGTTGTTTTGCTG
 GAAGGAGGGAGTGC GCGGGCTGCCCGGGCTCCTCCTGCCGCTCCTCTCAGTGGATGGTT
 CCAGGCACCTGTCTGGGGCAGGGAGGGCACAGGCCGTGCACATCGAAGGTGGGGTGGGACCA
 GGCTGCCCTCGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCGTGCCCTGCGACTCTCA
 GGGCTAAGGTCCTCTGTTGCTTTTGGTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT
 AGCTTGAAGGAGGACCAATG CAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCGCTG
 GCTCAGGCCTGCCCTGAGCCCTGCGACTGTGGGAAAAGTATGGCTTCCAGATCGCCGACTG
 TGCCTACCGCGACCTAGAATCCGTGCCGCTGGCTTCCCGCCAATGTGACTACACTGAGCC
 TGTGAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCTT CAGGGAGGTGCCCTGTCTGCAG
 TCGCTGTGGCTGGCACACAATGAGATCCGCAGGTGGCCGCGGAGCCCTGGCCCTCTCTGAG
 CCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGGCTGGAGCGACCTGC
 ACAACCTCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCG
 GACGCTTCCGCAGCCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACAC
 ATTGGCCGAGGGCACCTTCACCCCGCTCACCGCGCTGTCCCACCTGCAGATCAACGAGAACCC
 CTTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCCTGACCACGGCCGTGTCC
 ATCCCGGAGCAGGACAACATCGCTGCACCTCACCCCATGTGCTCAAGGGTACACCGCTGAG
 CGCGCTGCCGCATTCGCATGCTCGGGGCCCTCAGTGCAGCTCAGTCAACCAACGACGAGG
 ATGGTGCCGAGCTGCGGCCCTGGT TTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCG
 GCCCTCAGCTTCACTGGCACATCCAGATACCCAGTGGCAATTGTGGAGATCACAGCCCCAA
 CGTGGGCACTGATGGGCTGCCCTGCTTGGCACCCCTGTGGCCAGCTCCAGCCGCGCTTCC
 AGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC
 AGCTGCTGGCCACCAATGAGCTGGGCAGTGCTGAGAGCTCAGTGGACCTGGCACTGGCCAC
 GCCCGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAA
 AGGGCTGCTATACGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATC
 ATCTACCTCAGCCGTGCTGGGAACCC TGAGGCTGCAGTCGAGAGGGGTCCTTGGGCGAGCT
 GCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCCTCTTCTTCTCTCCTCACCCTCTCT
AGCCCCACCCAGGGCTTCCTTAACCTCCTCCCCTTGCCCTACCAATGCCCTTTAAGTGCTG
 CAGGGGTCTGGGGTTGGCAACTCTGAGGCCTGCATGGGTGACTTACATTTTCCCTACCTCT
 CCTTCTAATCTCTCTAGAGCACTGCTATCCCCAACTTCTAGACCTGCTCCAACCTAGTGA
 CTAGGATAGAATTTGATCCCTTAACCTCACTGTCTGCGGTGCTCATTTGCTGCTCAACGATTG
 CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCCTAATCCAAC TGGGAGAA
 GCCTCAGTGGTGGAATTCCAGGCCTGTGACTGTCAAGCTGGCAAGGGCCAGGATTGGGGGA
 ATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAGGAGGATGG
 GAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCT
 CCTTGCTGTTTTCTGATGATTTGGGGCTTGGGAGTCCCTTTGCTCATCTGAGACTGAAA
 TGTGGGGATCCAGGATGGCCTTCCTTCTCTTACCCTTCCTCCCTCAGCCTGCAACCTCTAT
 CTTGGAACCTGTCTCCCTTTCTCCCCAACTATGCATCTGTGTGCTGCTCCTCTGC AAAAGGC
 CAGCCAGCTTGGGAGCAGCAGAGAAAATAACAGCATTTCTGATGCCAAAAAAAAAAAAAAAAA
 AAGGGCGGCGCGACTCTAGAGTGCACCT

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FIGURE 12

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCA YRDLESVPPGFANVTTL SLSANRL
 PGLPEGA FREVPLQLQSLWLAHNEIRTVAAGALASLSHLKSLDL SHNLISDFAWSDLHNL SAL
 QLLKMSDNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPF DCTC
 GIVWLKTWALT TAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELR
 PGFVLALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTFVASSQPRFQAFANG
 SLLIPDFGKLEEGTYSCLATNELGSAESSVDVALATPPEGGEDTLGRRFHGKAVEGKGCYTV
 DNEVQPSGPEDNVV IYLSRAGNPEAAVAEGVPGQLPFGLLLLGQSLLLFFFLTSTF

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites.

amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site.

amino acids 319-326

N-myristoylation sites.amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,
334-340, 350-356, 394-400**Amidation site.**

amino acids 355-359

Leucine rich repeats.

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain.

amino acids 180-230

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FIGURE 13

CCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC
 AGCGCAGCAGAGTATCTGACGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGC
 AGCGAGGAGGTCTGAGCAGC**ATG**GCCCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT
 CTGGAGCATCCTCTGTGCTGCTGGCACTGCGGGCGAGGCCGGGCCGCCGAGGAGGAGA
 GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
 CTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTACAGAAAAGCGCAACAGAG
 AATGCCAGCTATTCCCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
 CAGAATACTTCTATGAATTCCTGTCTTGGCTCCCTGGATAAAGGCATCATGGCAGATCCA
 ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCCTCACAAAGGCATCAGTTGTTCAAGTTGGTTT
 CCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT
 CTGAAGGCAACACCATTTCCAAACACCTCAAAATGCTATCTTCTTTAAACATGTCAACAA
 GCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTG
 TCCTGATGGGTTCCACGGACCTCACTGTGAGAAAAGCCCTTTGTACCCACGATGTATGAATG
 GTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGT
 GACAAAGCAAAGTCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCCTGGAAAAATG
 TATTGGCCCTCCAGACTAGAGGGAGAGCAGTGTGAATCAGCAAATGCCCAACACCTGTC
 GAAATGGAGGTAATGCAATGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGGAGAC
 CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACATGGAACCTGCCATGAACCCAA
 CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC
 TCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGCAGCAGCCCTTCACTTAAAAAG
 CCCGAGGAGCGCGGGATCCACCTGAATCCAATTACATCTGGT**TGA**ACTCCGACATCTGAAAC
 GTTTTAAGTTACACCAAGTTCATAGCCCTTTGTAAACCTTTGATGTTGTAATGTTCAAAATAA
 TGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
 GATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGCTCTGTAGCATGATGGTATAGATTTTCT
 TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTCAGTG
 TGTAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGTGTCTGGGGCAGGGGAACAT
 CAGAAAGGTTAAATGGGCAAAAATGCGTAAGTACAAGAATTTGGATGGTGCAGTTAATGT
 TGAAGTTACAGCATTTAGATTTTATTTGTGATATTTAGATGTTTGTACATTTTAAAAAA
 TTGCTCTTAATTTTAAACTCTCAATACAATATATTTGACCTTACCATTATTCAGAGATT
 CAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTTAACAATATAATATATCTA
 AACACAATGAAATAGGGAATATAATGTATGAACCTTTTGCATTGGCTTGAAGCAATATAATA
 TATTGTAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT
 AAAGGTGCTGCTTTAGTTTTTTGGAAAAA

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FIGURE 14

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGG
 MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLSLSLDKGIMADPTVNVPLL
 GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIMNSEGNTILQTPQNAIFFKTCQQAECPGGC
 RNGGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
 TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKIGKSKCKCSKGYQGDLCSKPVC
 EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
 PESNYIW

Signal sequence.

amino acids 1-28

N-glycosylation sites.

amino acids 88-92, 245-249

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPWTWVRSYEFTSNCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

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FIGURE 17

CGGAGAACCTTTTGACGCGCACAACTACGGGGACGATTTCTGATTGATTTTTGGCGCTTTCGATCCACCCCTCC
TCCCTTCTC**ATGGG**ACTTTGGGGACAAAGCGTCCGGACCGCCTCGAGCGCTCGGAGCAGGGCGCTATCCAGGAGC
CAGCAGAGCGTGGGGAACCAAGCATGGCTCCTGGACCCCAAGATCCTTAAGTCTCGTGTCTTCATCGTCCGGG
TTCGTCTCGCGGTCCGGGTGTACTGTGCCACCATCCCCCGGACGAGCAGAGTTCCCCAGCAGACAGTGGGCCCA
CAGCAACAGAGGCGCAGGCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCGTG
TACCCTGTGCAGAGGGGTGGATTACACCATTGCTTCCAACAATTTGCCTTCTTGCTGTCTATGACAGGTTT
GTAAATCAGGTCAAACAATAAAGTTTCTGTACCACGACCAGACACCGGTGTGCTAGTGTGAAGGAGGAAGC
TTCAGGATAAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTTCAG
TAATTTGACGCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAAACCCAGCAG
CGGAGGAGACAGTGACCACCATCTCGGGATGCTTGCTCTCCCTATCACTACCTTATCATATAGTGGTTTTA
GTCATCATTTTAGCTGTGGTTGTGGTTGGCTTTTCATGTCCGAAGAAATTCATTTCTTACCTCAAAGGCATCTG
CTCAGTGTGTGGAGGAGTCCCGAACGTGTGCACAGAGTCCTTTCCGGCGCGCTTCATGTCTTCACGAGTTT
CTGGGCGGAGGACAATGCCCGAACGAGACCTGAGTAACAGATATCTTGACGCCACCCAGGTCTCTGAGCAG
GAATCCAGGTCAGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCCGACAGAGGAGCCACAGCGTCTGT
GGAACAGGCAGAAGCTGAAGGTTGTGAGAGGAGGCTGCTGGTCCAGTGAATGACGCTGACTCCCGCTGACA
TCAGCACCTTGCTGGATGCTCGGCAACACTGGAAGAAGGACATGCAAAAGGAAACATTCAGGACCAACTGGTG
GGCTCCGAAAAAGTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCTGCCCTG**CA**AAAGAAATCTCTTCAG
GAACACAGAGCTTCCCTCATTTACCTTTTCTCCTACAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGA
CCCATGCCCAACAAACTCTACTATCCAATATGGGGCAGCTTACCAATGGTCTTAGAACTTTGTTAACGCACCTT
GGAGTAATTTTATGAATACTCGCTGTGATAAGCAAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGT
TATACGATTGTGTATTAAGGTCGTTTTAGGCCACATGCGGTGGCTCATGCCCTGAATCCCGACAGCTTTGATAG
GCTGAGGCAGGTGGATTGCTTGAGCTCGGGAGTTGAGACCAGCCTCATCAACACAGTGAAACTCCATCTCAAT
TTAAAAAGAAAAAAGTGGTTTAGGATGTCTCTTTGCAAGTTCTTCATCATGAGACAACTTTTTTTCTG
TTCCTATATTGCAAGCTCCATCTCTACTGGTGTGTGCAATTAATGACATCTAATACAGATGCCGACACGCCAC
AATGCTTTGCCTTATAGTTTTTAACTTTAGAACGGGATTATCTTGTATTACCTGTATTTTCAGTTTCGGATA
TTTTTGACTTAATGATGAGATTATCAAGACGTAGCCCTATGTCTAAGTCATGAGCATATGGACTTACGAGGGTGT
GACTTAGAGTTTTGAGCTTTAAGATAGGATTATTGGGGCTTACCCCAACCTTAATTAGAGAAACATTATATTG
CTTACTACTGTAGGCTGTACATCTCTTTCCGATTTTGTATAATGATGTAACATGGAAAACTTTAGGAAAT
GCATTTATTAGGCTGTTTACATGGGTTGCCTGGATACAAATCAGCAGTCAAAATGACTAAAAATATAACTAGT
GACGGAGGGAGAAATCCTCCCTCTGTGGGAGGCATCTACTGCATTCAGATTCTCCCTCCTGGCCCTGAGACT
GACCAGGGTTTGTAGGCTGGCAGCTTCTCAAGGGGAGCTTGCTTACTTGTATTTTAGAGGTATATAGCCA
TATTTATTTATAAATAAATATTTATTTATTTATTTATAAGTAGATTGTACATATGCCAGGATTTTGAAGAGC
CTGGTATCTTTGGGAAGCCATGTGCTGGTTGTGCTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTC
CTCAGCAGATGAGGACAGTGAGAATTAAGTTAGATCCGAGACTGCGAAGAGCTTCTCTTTCAAGCGCCATTA
GTTGAACGTTAGTGAATCTTGAGCCTCATTTGGGCTCAGGGCAGAGCAGGTGTTTATCTGCCCCGCGATCTGCC
ATGGCATCAAGAGGGAAGAGTGGACGGTGCTTGGGAATGGTGTGAATGGTTGCCGACTCAGGCATGGATGGGC
CCCTCTCGCTCTGTGGTCTGTGAATCAGTGCCTGGGATGCCTTTTAGGGCAGAGATCTCTGAGCTGCGTGT
TAGGGTACAGATTCCCTGTTTGAAGAGCTTGGCCCTCTGTAAGCATCTGACTCATCTCAGAGATATCAATCTT
TAAGACTGTGACAACGGGATCTAAATGGCTGACACATTTAGCCTGTGTACGCTTCCATTATTTTATTTAAA
AACCTCAGTAATCGTTTATAGCTCTTTCCAGCAAATCTTCTCCACAGTAGGCCAGCTGTGGTGAAGTAAATTA
CGCATATAGTCATCTAAGGGGTTTCAGTCTTTCCATCTCAAGGCATTTGTGTGTTTCCGGGATGGTTT
GCTGGGACAAAGTTAGAAGTGCCTGAAGTTCGCACATTCAGATTGTTGTGTCCATGGAGTTTTAGAGAGGGATG
GCCCTTCCGGTCTTCGCACTCTGCATCTCCACTTCCATCTGGCCTCCACACCTTGTCCCTCGACTCTCTG
GATGACAGAGGGTGTCTGCTGCTTCTAGTCTTGTGCTTGTGGGCCCTCTGTGTCAGGAGACTTGGCTCAAAG
CTCAGAGAGAGCGACTCGGTGCCGCTCCTTTGTCCCTTCTCAGAGGCCCTTCTTGAAGATGCATCTAGACT
ACAGCCTTATCAGTGTTTAAGCTTATCCCTTAAACATAAGCTTCTGACAACTGAATTTGTTGGGGTTTTT
GGCGTTGGTTGATTTGTATTAGGTTTTGCTTTATACCCGGGCCAAATAGCACATAACACTGTGTATATATGAAA
TACTCATATGTTTATGACCAAAATAAATATGAACCTCATRTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 18

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQD
 EVPQQTVAPQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG
 QTNKSSCTTTRDTCVQCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAA
 SSTGKTPAAEETVTITLGLASPYHYLIIIVVLVII LAVVVVGFSCRKKFISYLGKICSGGG
 GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAELTGVTVES
 PEEPQRLLEQAEAEQCRRLRLVPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKL
 FYEEDEAGSATSC

Important features of the protein:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,
 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

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FIGURE 19

GCGGCACCTGGAAGCATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAAGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAATGAATGGAATTCCTTAAAAAAAAA

amino acids 81-87, 108-114, 119-125

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FIGURE 21

CCGGGGAGGGGAGGGCCCGTCCCGCCCTCCCCGTCTCTCCCCGCCCTCCCCGTCCCTCCC
GCCGAAGCTCCGTCCCGCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCCGGCTGCCCTC
TGCCCGGGTTGTCCAAGATGAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG
TTCGTGGCGCTACCCGCTCCGGCTGGCTGACGACGGGCGCCCCGAGCCGCCGCGCTGTC
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAACACTACACTGAAAGATGATGGGGACATAT
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA
CCTGTAAATAGTGGTGTAAACCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT
TGAAAATTTGGAGGAAAAAGAATATTTTGGAAATGTCAGTGTAAGGATTTTAGTTCATGAGT
GGCCTATGACATCTGGTTCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
GATGGAAAACAAGTTCAGCAAAAGGATGTCAGTGAATTTGATATTTTAGTTAAGAACCGGG
AGTACTCAGACATTCAACTATACCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTCTC
GAGACAGTGACATTTTATTTACCTTCCTAACCTCTCCAAAAAGAAAGTGTTAGTTCAGTG
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAAACCACTGTAGATGAAGATGTTTACC
TGGCAAGTTACCTGAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTCCAGTATTC
TTTCAGTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT
AAAGGTGTTTTTCCAGTTTCTGAATACAAAGGAATTCTTCAGTTGGATAAAGTGGACGTCA
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA
GATAAACATGTATTTAAACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC
AAATTTGCCACTTGAATATAATTTCTTTAAATCGTT

22/75

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGLALRLLLFVALPASGWLTTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQKQDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRSDIL
FTLPNLSKKESVSSLQTTSQYLIRNVETTVDVLPGLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAADVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPEKRAENLEDKTCI

Important features of the protein:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

FIGURE 23

CGTCTCTGCGTTCCGCCATGCGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGG
 CCCTGGCTTGGGCGGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCGTTGGT
 GTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACATGATGTCAC
 CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGG
 GGAACAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAGATTCG
 TGCAGCGGGCGTGGAGTGCGGCCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCGCGTGC
 CGAGTGCGCCGCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCG
 CCACCTACCGCGACAGTGCAGCTGCGCGCGCGCGCTGCCCGGCCACCCGGACCTGAGC
 GTCATGTACCGGGGCGCTGCCGCAAGTCCTGTGAGCACGTGGTGTGCCCGCGGCCACAGTC
 GTGCGTCTGTGGACCAGACGGGCGAGCGCCACTGCGTGGTGTGTGAGCGGGCGCCCTGCCCTG
 TGCCCTCCAGCCCCGGCCAGGAGCTTTGCGGCAACAACAACGTCACTACATCTCCTCGTGC
 CACATGCGCCAGGCCACCTGCTTCTTGGGCGCTCCATCGGCGTGCGCCACGCGGGCAGCTG
 CGCAGGCACCCCTGAGGAGCGGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAACTTCGTGT
GAGCCTGCAGGACAGGCCTGGGCTGGTGCCCGAGGCCCCCCATCATCCCTGTTATTATT
 GCCACAGCAGAGTCTAATTATATGCCACGGACACTCCTTAGAGCCCGGATTCCGAGCACTT
 GGGGATCCCAAGCCTCCTTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCGCTGGGGGCC
 GGCTGGTGGTGGGATAGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT
 AGGATGCCCCAGGCCCTACCCTAAGACCTATTGCGGGGGAGGATTCCACACTTCCGCTCCTT
 TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGTGGTAATT
 CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGT
 CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGAGGATCTAG
 TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGAGGATCTAG
 CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG
 GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG
 GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCCTGTGGGGA
 CCTCAGAACACTGTGACCTTAGCCCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC
 CACCATTCCCTGCCAGCCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT
 CCTGTGAAGGCCATTGAGAAATGCCCAGTGTGCCCTGGGAAAGGGCACGGCCTGTGCTCC
 TGACCGGGCTGTGCTTGGCCACAGAACCACCCAGCGTCTCCCTGTGCTGCTTCCACGTCAG
 TTCATGAGGCAACGTGCGTGGTCTCAGACGTGGAGCAGCCAGCGCAGCTCAGACGAGGGC
 ACTGTGTCCGGCGGAGCCAGTCCACTCTGGGGGAGCTCTGGCGGGACCAAGGCCACTGCTG
 TCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT
 CCTGGAGCCGGGTGTCCCAGTGGCACCACTAGGTGCCCTGCTGCCCTCCACAGTGGGGTTTACA
 CCCAGGGCTCCTTGGTCCGCCACAACCTGCCCCGGCCAGGCCTGCAGACCCAGACTCCAGCC
 AGACCTGCCCTACCCACCAATGCAGCCGGGGTGGGCAACCCAGCCAGGTGCTGGTCTTGGG
 CCAGTTCTCCCAAGCAGGCTCACCTCCCCTCCATCTGCGTTGATGCTCAGAATCGCTACC
 TGTGCCTGCGTGTAAACCACAGCCTCAGACCAGCTATGGGGAGGACAAACCGGAGGATAT
 CCAGTCTCCCCGGTCTGGGGTGAAGAAATGTGGGGAGCTTGGGCACTCTCTCCAGCCTCCTC
 CAGCCCCAGGCAGTGCCTTACTGTGGTGCCCAAGAAAGTGCCTTAGTGTGGTGGGTCTA
 CAGGAGCCTCAGCCAGGCAGCCACCCACCCTGGGGCCCTGCCTACCAAGGAATAAAGA
 CTC AAGCCATAAAAAAA

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FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGFVSSMSGNPAAGGVCWLQQQEATCSLVLQTDVTRAEC
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGPRCECAPD
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCKRSCEHVVCPRPQSCVVDQ
TGSAHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEEENFV

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

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FIGURE 25

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGTGCTGGGGT
TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT
AAAATCGCGATTATTGGAGCCGAATTGGTGGCACTTCAGCAGCCTATTACCTCGGCAGAA
ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGTTCGGGGGCCGCTTGCTA
CCATGATGGTGCAGGGGCAGAATACGAGGCAGGAGGTTCTGTCTATCCATCCTTTAAATCTG
CACATGAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACT
GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA
TTAAATTAGTTTGGCGCTATGGATTTCATCCCTCCGTATGCACATGTGGGTAGAGGACGTG
TTAGACAAGTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGA
AAAACTACTTCATGCTCTAGGAGGAGATGACTTCCTTGGAAATGCTTAATCGAACACTTCTTG
AAACCTTGCAAAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATG
AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGCGGTGTCACTGTCTGTG
TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCCTAGGGCTTCTGC
AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACC
AAGTACACAGGAAATCCACAAAGATGTATGAAGTGGTCTACCAATTGGAAGTGTGAGACTCG
TTCAGACTTCTATGACATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTGGAATATTA
CTTTTCTCACTTTGATCCTCCAATTGAGGAATTCATCAATATTATCAACATATAGTGACA
ACTTTAGTTAAGGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAAATTTGG
CCTTAATACAGTTTTAACCACTGATAATTGAGATTTGTTTCATTAACAGTATTGGGATTGTGC
CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGGGAAGATC
TTTTCCCAAGAACTCTTACTAAAGCACAAATTTTAAAGCTCTTTCTGTCTCTATGATTATGC
TGTGAAGAAGCCATGGCTTGCAATCCTCACTATAAGCCCCCGGAGAAATGCCCTCTATCA
TTCTCCATGATCGACTTTATACCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATG
AGTGCCATTGCAGCCACAAACGCTGCACTCCTTGCTATCACCGCTGGAACGGGCACACAGA
CATGATTGATCAGGATGGCTTATATGAGAACTTAAACTGAACATTGAAGTGACACACTCC
TTTTTCCCCTCCTAGTTCCAAATGACTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGA
TGATTTTGAAACAGATATTTGCCATTATCATGTTTAATAAAAGTAATCCCTGCTGGTCAAT
AGGAAAAAAAAAAAAA

26/75

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880

<subunit 1 of 1, 505 aa, 1 stop

<MW: 56640, pI: 6.10, NX(S/T): 4

MGRVVAELVSSLLGLWLLLCSCGCEGAELRAPDKIAIIGAGIGGTSAAYYLRQKFGKDVK
IDLFEREVEVGRLATMMVQGQYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGE
TLVFEESNWFIINVIKLVWRYGFQSLRMHMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHAL
GGDDFLGMLNRTLLETLOKAGFSEKFLNEMIAFVMRVNYGQSTDINAFVGA VSLSCSDSGLW
AVEGGNKLVC SGLLQASKSNLISGSVMYIEEKT KTKYTGNPTKMYEVVYQIGTETRSDFYDI
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFG LNTVLT
TDNSDLFINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKFLSYDYAVKKPWL
AYPHYKPEKCP SII LHDRLYYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDG
LYEKLKTEL

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

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FIGURE 27

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGAC**ATG**AT
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAGACTTATTCAGTCAGAGCTAT**TAA**
GAGATGATGGAAAAAGCCTTCACCTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAATAAATGTTTTTTAAATCTGA

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FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEGLFYAQSKKKPL
MVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP
SLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

Important features:**Signal peptide:**

amino acids 1-23

N-myristoylation site.

amino acids 51-57

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FIGURE 29

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCAGCCATCTTGGA
GTGGCTGTTGGTTTCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTGTGTTCCCTTACCCATATCCATTTGCGCCACTTCCAC
CAATCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

30/75

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPERPLPPIPFPRFP
WFRNFPPIPIPESAPTTPLPSEK
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

FIGURE 31

CGGACGCGTGGGCGGGCGCGCCGGAGGGACCGGCGCGGC**ATG**GGCGGGGGCCCTGGGAT
 CGGGGCCCCGTCTCGCCCGCTGCTGCGCGCTGTGTGCTGCTGCGGCTGGCCCGGCGCGCGCG
 GGGAGCGCCGGGGCCCGACGGTTTAGACGTCTGTGCCACTTGGCCATGAACTGCCACATGCC
 AGCAAAGAGAAGGGAAGAAGATCTGTATTGTGCAACTATGGATTGTAGGGGAACGGGAGGACT
 CAGTGTGTTGATAAAAAATGAGTGCCAGTTTGGAGCCACTCTTGTCTGTGGGAACCCACACATC
 TTGCCACAACACCCCGGGGGCTTCTATTGCAATTGGCCTGGAAGGATATCGAGCCACAACA
 ACAACAAGACATTATTCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT
 TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG
 TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCACCCCGACCCAGATGCCACAT
 CATGCACAGAAATAGACTGTGGTACCCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT
 TATACGTCTAGTCTGGGCGAGCCAGGTTTCGTTATGCTTGAGAGAAGGATCTCTTCAAGTPTCC
 AGAAGATACAGTTTCAAGCTGCACAGGGCTGGGCACATGGGAGTCCCCAAATTACATTGCC
 AAGAGATCAACTGTGGCAACCTCCAGAAATGCGGCACGCCATCTTGGTAGGAAATCACAG
 TCCAGGCTGGGCGGTGTGGCTCGCTATGCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA
 GATCACTTCTGTTTGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAATCATGCACAGAAA
 TTCTGCAGAAAGATTAAATGATATCACTGTTTGAATGATACCTGTGTAGATGGCAAAATTAAC
 TCAAGAAGATAAACCCCAAGATCTCATATGTGATATCCATAAAAGGACAACGGTTGGACCC
 TATGGAATCAGTTCGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGAGCCCAAGAGTGT
 GCCTAGCCCTGTATCCAGGCACCAACTACACCGTGAACATCTCCACAGCACTCCAGGCGC
 TCGATGCCAGCCGTCATCGGTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG
 TTTCAATATTTCAATATTTAATGAACTTGTGTTGAATTGAACTGACAGGCGTTAGCGAAGTGTG
 GATCAGAACACATGTACCAATTTACCGTTCTGGGTGAGAGTGGTATCTCGCTAACTTTTCT
 CATGCAACATCGTTTAACTTCACAACGAGGGGAACAAGTGCCTGTAGTGTGTTGGATCTGTA
 CCTACGACTGATTATACGGTGAATGTGACCTGCTGAGATCTCCTAAGCGGCACTCAGTG
 AAATAACAATAGCAACTCCCCAGCAGTAAAAACAGACCATCAGTAACATTTTCAAGATTAAAT
 GAAACCTGCTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGTAATTTATTTCCA
 CATTTTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCAGGAAATGACCTTTAATATCAGTA
 CGACAGCCGAGATCCCCAGGTGTGCTTGGACCTACGTCGGGTACCAACTACAATGTCAGT
 CTCGGGCTCTGTCTTCGGAACCTTCCTGTGGTCATCTCCTGACAAACCCAGATAAACAGGCC
 TCCCTCTCCGGAAGTAGAATTTTTTACGGTGCACAGAGGACCTCTACAGCCCTCAGACTGA
 GGAAGCCAGGAGGAAAAATGGACCAATCAGTTTATATACAGGTGTTAGTGCTTCCCTGGCC
 CTCCAAAGCACATTTTCTTGTGATTTCTGAAGCGCTTCTCTCTTCTTTAGCAACGCCCTCTGA
 TGCTGATGGATACGTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA
 TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATAATGCACTTTGAAAAGAGGGAGT
 GATTACTGCATTATATTACGAATCACAAAGTGAATGGAATAAGGTGAGAAGACACTCTCTGTGC
 AGTTTGGGCTCAGGTGAAGATTCGTCACTCATGTCTGCAGATGAGCGGGTGTGGACTGG
 GTTCCCTGGCTGTGTGATCATTTCTCACATTTCTCTCTCTCTCAGCGGTG**TGAT**GGCAGATG
 GACACTGAGTGGGGAGGATGCACTGCTGCTGGGCAGGTGTTCTGGCAGCTTCTCAGGTGCC
 GCACAGAGGCTCCGTGTGACTTCCGTCCAGGAGCATGTGGGCGCTGCAACTTTCTCCATTCC
 CAGCTGGGCGCCATTCCTGGATTAAAGATGGTGGCTATCCCTGAGGAGTCAACCATAAGGAGA
 AAACCTCAGGAATTCAGTCTTCCCTGCTACAGGACCAAGTCTGTGCAATGCAACTTGAGACT
 CCTGATGTACACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGAC
 TTCTCTGAGTGATGCCTGAGGCTCAGTCTCTTAGACATTTGACTGCAAGAGAATCTCTGCA
 ACCTCCTATATAAAAGCATTCTGTGTTAATTCATTCAAGATCCATTCTTTACAATATGCAATG
 AGATGGGCTTAAGTTTGGGCTAGAGTTTGACTTTATGAAGGAGGTCATTGAAAAAGAGAAC
 GTGACGTAGGCAAAATGTTTCAAGCACTTTAGAAAACAGTACTTTTCCATAAATTAGTTGATAT
 ACTAATGAGAAAATATACTAGGCTGGCCATGCCAAATAGTTTCCGTGCTGTCTGTTAGGCA
 GCATTGCTTTGATGCAATTTCTATTGCTCATATATTCAAAGTAATGTCTACATTCAGTA
 AAAATATCCCGTAATTAAAAA

[illegible]

FIGURE 32

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pI: 6.36, NX(S/T): 18
MGRGPWDAGPQSRRLPLLILLGLARGAAGAPGPDGLDVCATCHEHATCQQRREGKKICNICYG
FVNGRTQCDVKNCEQFATVLGNGNTHSCHNTPGGFYICLEGYRATNNKTFIPNDGTFTCT
DIDCEVSGLCRHGGRCVNHGHSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPPEVPD
DGYIIGNYTSLSGSQYVACGEGFESVPEDTVSCTGLGTWESPKLHCQINCGNPPMRNDI
ILVNGNHSRLGQVARYVCQGFESPGGKITSVTEKGTWRESTLTTEILTKINDVSLFNHDT
CVRWQINSRRINPKISVISIKGQRLDPMESVREETVNLTTDSRTPEVCLALYPGTNYTVNI
STAPPRRSMPIAVIGFQAEVLDLDDGSFNISIFNETCLKLNRSRKRVSGEHMYQFTVLGQR
WYLANFSHATSNFTTREQPVVCLDLVPTTDDYVNTVLLRSRQVQITIAATPPAVKQTI
SNISGFNETCLWRSLIKTADMEEMYLFHWGQWRQYKEFAQEMTFNISSSSRDEPEVCLDLRP
GTYVNSLRLASSELSPVADISLTTQITEPLPEVEEFFTVHRGGLPRLRLRAKEKNGPSISSY
VLVLPALAQSTFSCDSEGASSFTSNASADAGYVAEALLAKDVPDAMEIPIGRLYYGEYYN
APLKRGSDDYCIILRITSEWNKVRRHSCAVWAQVKDSSLMLLMQAGVGLGSLAVVIILTFLSF
SAV
```

Important features of the protein:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 718-740

N-glycosylation sites.

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352, 367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474, 498-502, 503-507, 542-546, 563-567, 645-649

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 478-482, 686-690, 705-709

Tyrosine kinase phosphorylation site.

amino acids 419-427

N-myristoylation sites.

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126,
146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694,
727-733.

Amidation site.

amino acids 52-56

Aspartic acid and asparagine hydroxylation sites.

amino acids 91-103, 141-153.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 624-635

Cytochrome c family heme-binding site signature.

amino acids 39-45

Calcium-binding EGF-like domain proteins pattern proteins

amino acids 85-106, 135-156

Receptor tyrosine kinase class V proteins:

amino acids 389-422

FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGGATG
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAAAGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCCGGGCCACGCCGCTCTGGAAGCTCAAACGCTGAGCGTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTACAAAAACATCTCCAACTTCATGTTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTTCACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
 GTCACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTCCAGCATCCCTGGGGCTCAGA
 CATAGATCTCATCCCCACGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCGTGTCC
 ACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTGTGAGACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTACCC
 CTTCAGAGACACGGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACGTGAGTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCCACGCGCCTCACTTCCAGGTCTCTTACTGCGTGTCAGGAGAGGCTA
 ACGGACATCAGCTCAGCCAGGATGTCCCGTATGCCAAAAGAGGCTGTGCCCTTAGCCTG
 GGCCCCACCGACAGACTGCAGTGCCTTACTGTGTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCACTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTCGCA
 TTAAATTCACTCAGTGTGGCCCAAAAAA

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FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722
><subunit 1 of 1, 482 aa, 1 stop
><MW: 49060, pI: 4.74, NX(S/T): 4
MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSEA
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
TTVQITITGSDPEEAI FDTLCTDDSSEEAKLTMDILT LAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNI
EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNETPSETPTMDIATKGFPTSRD
PLPSVPPTTNSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

N-myristoylation sites.amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
314-320, 349-355, 386-392, 397-403, 449-455**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

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FIGURE 35

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCGGTCTGACAGCCACTCCAGAG
GCCATGCCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCTGTTAATTCTGGCTTTGGGCCA
GGCAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC
CCCAGAAGTTC AACCTGTGCCTTATATCTTGAAGAAAATTTCCAGGATCGCAGGCAGCA
GCGACCAC TGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGAATGT
ACTTCGCTTCTCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
TTGGCCCAGCTGGGCTGGACTTGGGGCCCAATTCCTACTATAACCTGGGACCAGAGCTGGA
ACTGGCTCTGTTCTCGGTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA
AAATGTTTGTGTTGCGGTCACTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT
GTAGCTAAGGATTGGAATGACAACCCCGGAAAAATTTGGGTTTATTCCTGGAGATACTGGT
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT
GCTCCCTTCATGCTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCCTTCTCGG
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTCTTGTGAAGAACCTCTGCCACCGTCACCA
GCTATTATTAACCTCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTTCA
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT
TATGCTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCAGGCTGTGTGTAT
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAAGACAATAATGACAATGTCTATTCTAC
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAAT
AGAAGGAGTGTTCTTAGGGTAAATCTTTTAATAAACTACCTATCTGGTTTATGACCCTTA
GATCGAAATGTC

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FIGURE 36

MLRFLPDLAFSFLILALGQAVQFQXYVFLQFLGLDKAPSPQKFQPVPIYLKKIFQDREAAA
 TTGVSRLDCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL
 AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRSPVPQGAHVFNLLDV
 AKDWNNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRK
 RRAAIPVVKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPFSLTISLNSSNY
 AFMQALMHAVDPEIPQAVCIPTKLSPISMLYQDNNNDNVILRHYEDMVVDECGCG

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

FIGURE 37

CACTTTCTCCCTCTCTTCCCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
 CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTTGGCTGCTCGTA
 CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTCCCTGCTCTGTT
 TCCTTACCAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
 TGCTCTAGGGGGCGCGGGGAGGAGCGCCGGCGGGACGGAGGGCCCGCAGGAAGATGGGC
 TCCCGTGGACAGGGAATCTTGTGGCGTACTGCTGCTTGCCTTGGCTTGGCTGCTGCTGCT
 CCTGAGTCGTGTGCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
 CGTCGCTCCCGACCATGCCGAGGGGCTGAAGAACACATGAAAAATACAGGCCAGTCAG
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC
 GGCACCGCCGTGCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
 ATCAGGGCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
 CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
 CTTTTCGGTGGGCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
 ACACGGAGTTTCGTAACCTCTACGACCACTTCAACATGTTACCCGGCAAGTTCTACTGCTAC
 GTGCGCCGCTCTACTTCTTACGCCTCAACGTGCACACCTGGAACAGAGAGACACTACCT
 GCACATCATGAAGAACGAGGAGGAGGTGCTGCTTGTGCGCAGGTGGGCCAGCCGACGA
 TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACAGGTGTTGGTACGCCTC
 TACAAGGGCGAACGTGAGAACGCCATCTTACGCGAGGAGCTGGACACCTACATCACCTTCAG
 TGGCTACCTTGGTCAAGCAGCCACCGAGCCCTAGCTGGCCGGCCACCTCCCTTCCCTCTGCC
 ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGCATCCCTGGACTCCGACTC
 CCTGGCTTTGGCATTAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCATCGGTCTCC
 CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAATCACCAGGGCGGGCACCCGC
 GAGAACCCTCTGGGACCTTCCCGGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCAGGGC
 GAGACGCGGGTGCGGCAGGGCGTCCCAGGGTGCGGCACCCGCGGCTCCAGTCTTGGAAATA
 ATTAGGCAAATTTCAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAGGG
 TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCTTTTCAGTTGAG
 ACTCTGCTTAAAGAGAAGATCAAAGTTAAAGCTCTGGGCTCAGGGGAGGGGCCGGGGCAGG
 AAACCTACCTCTGGCTTAAATTCCTTTAAGCCACGTAGGAACCTTCTTGGGGATAGGTGGACC
 CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGCTCTTCTGAGTCACAGCTGCGAGGT
 GATGGGGCTGGGGCCCCAGGGCTCAGCCTCCAGAGGGACAGCTGAGCCCTGCTTGGC
 TCCAGTTGGTGAAGCAGCCGAAGGGCTCTGACAGTGGCGAGGACCCCTGGGTCCCCCA
 GGCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
 ACCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCCTGGCATCGGCT
 TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTCTGTGTTTTT
 TATAAAACACCTCAAGCAGCATGCACTCTCCATCTCCTGTGGGCTAAGCATCACCGCTT
 CCAGTGTGTGTGTTGGTGGCAGCAAGGCTGATCCAGACCCCTTGTGCCCCACGCTCCT
 CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTACAGCAGGGGAGAG
 CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTGTG
 AGACCAGAGTCAAGAGGAAGTACACGTCCTCAATCACCGTGTGAGGATCACTCTCAGGAGC
 TGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATTGCAGGACCACTGGAGAGGGGTGCG
 GTGCTGCCACGGTGTCTCGCCCTGCCATGGCCACCCAGACTGTATCCAGGAACCCCA
 ATAGCCCTTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTGTATCCCGCTGGGCC
 CCCAAAGCCCGCTGCCCTCTCTTCTTCCCCCATCCCCCACTGGTTTTGACTAATCCTGT
 TTCCCTCTCTGGGCTTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACT
 CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCTGCCCGGAAGCAGAGCCCACTC
 GCTGCTTAAGCTCCCCAGCTCTTCCAGAAACATTAACTCAGAATTGTGTTTTCAA

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FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELSPFDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDGRGLQGKYGKTGSAGARGH
TGPKGQKGSMSGAPGERCKSHYAAFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 39

GAATTCGGCACGAGGGAAGAAGAGAAAGAAAATCTCGGGGCTGCTGGGAGCATATAAGAA
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGAC**ATGG**CTG
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCGGTCCCTGT
GACACTCAAGAGCTACGATGCTGTGTATTTCAGGAACACTCTGAATTCATTCCTCTCAAACT
CATTAATAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG
TCCCAAAAATGGGAGTATGATTTGTTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT
GGCCCAATTACTAACAGGTTCCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGCAAT
GAAGCTTCTGTATAGTGTGAGCATGAAAAGCCTCTATATCTTTTCATTTGGGAGACCTGAGA
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC
AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCC**TA**
AAAGCCACTCATGAGGCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTGGCGTTCTCA
TTCTTATACTCTATTCGGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT
TATTATAAATGTTTTATTACTTAACCTCCTAGTGAATGTTACAGGTGACTGCTCCCCCAT
CCCCATTTCTTGATATTACATATAATGGCATCATATACCCCTTTATTGACTGACAACTACT
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG
TGCATCTCGGTGTAGAGCAAGGCTCCTTGTCTTCAGTGCCCCAGGGTGAATACTTCTTTGA
AAAATTTTCATTCATCAGAAAATCTGAAATAAAAATATGTCTTAATTGAG

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FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSEFIPLKLIKINIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPAMKLLYSVEHEKPLYLSFGR
PENKRIFPFFIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

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FIGURE 41

CAGAC**ATG**GCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC
AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT
TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG
CTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAAGGCTGCA
AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCAT**TAG**CCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCACCAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG
CTCAGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCCACTCTTTCTCCTGCTTTAAC
CACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCTGCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGAGGGAGAGTCTCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCCT
TGAAGGAGAATCATCAGGACCTGGACCTGATACGGCTCCCAGTACACCCACCTCTTCCT
TGTAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCCNCCCA

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FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLLILVLAFGIPTQSGDGAQDCCLKYSQRKIPAKVVRSYRKQEPSLGCSIPAI
LFLPRKRSQAELCADPKELWVQQLMQHLDKTPSPQKPAQGCRKDRGASKTGKKGKSGKCKR
TERSQTPKGP**Important features of the protein:****Signal peptide:**

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

FIGURE 43

AAGGAGCAGCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCATATCCTGTCCACATTGGAGACTCTGCAGATCATTAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTCTCTTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGAT**GACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGCCTGCAGGCCATCCTGGGAGTAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTACCTATGA

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FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 45

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCTCCCGAAACCCGGCCG
 CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA
 CAAGAAGCCGCCCTGCTGCCCGGGCCGGGGAGGGGCTGGGGCTGGGGCCGGAGGCGG
 GGTGTGAGTGGGTGTGTGCGGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGCACCTACCCGTGGGGGCGCTAAGGCGCTACTATATAAGGCTGCCGGCCGGAG
 CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACCTCACAGCCCCGAGCGCATCCCGGTGCGCGCCGAGCCTCCCGCACCCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGATAGG
 ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
 ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGCTCGTGGACTGCGCGCGGGGC
 CAGAGCGCGCACAGTTTGTGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
 CGTGACACGCTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGACGGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
 TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTTTCTTCCACTCTCTCATTTTCTGCCCATGCTGCCATGGTCCAGAGGAGCCTG
 AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG
 GACCCATTTGGGCTTGTACCCGACTGGAGGCGGTGAGGAGTCCCAGCTTTGAGAAGTTAACT
 GAGACCATGCCGGGCCCTTCTACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAACAGTCCTGAGTCCACGTTTCTGTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGATACATATTCAGAGTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
 CATAACATTGTAAGCTGTAGCTTGCCAGCTGCTGCTGGGCCCCATTCTGCTCCCTCGA
 GGTGTCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
 TCACTTCCTTTGGAAAAATCTTATGTCAAGCTGAAATTCCTAATTTTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAGGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAAGTGAAGTGGAGCAGGCATGGCCACCAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
 CTGAGGCCAGTTCTGTGATGGATGCTGTCTTGAGAATAAATTGCTGTCCCGGTGTCACTGTC
 TTCAATCTCCAGGCCACAGCCCTCTGCCACCTTCACATGCTTCCCATGGATTGGGGCCT
 CCCAGGCCCCCAGCTTATGTCAACCTGCACCTCTTGTTCAGAAATCAGGAAAGAAAGAT
 TTGAAGACCCCAAGCTTTGTCAATAACTTGCTGTGTGAAGCAGCGGGGGAAGACCTAGAAC
 CCTTTCCCGAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATTTATTTATGCCCCAAATTATATTTATGTATGTAAGTGAGGTTG
 TTTTGTATATTAAATGGAGTTTGTTTGT

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FIGURE 46

MRSGCVVHVHILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 47

GTCTGTTCCAGGAGTCCCTTCGGCGGCTGTTGTGTCACTGGCCTGATCGCGATGGGGACAAA
 GGGCGAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
 CATTGGGCAGTGTTACAGTGCCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
 GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCGTGTGGAGTGGAAGTTTGACCA
 AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACGGG
 TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
 ACTTGATGGTCTCTGAGGAAGCGGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
 GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGG
 CAGTGCTGACATGCTCAGAACAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
 GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
 GAATCCCACAAACAGGAGAGCTGGTCTTTGATCCCCGTGCAGCCTCTGATCTGGAGAATACA
 GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
 GTGGAGCGGAATGTGGGGGTATCGTGGCAGCCGTCTTGTAAACCTGATTCTCCTGGGAAT
 CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGACAAAGAAAGGGA
 CTTGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTAAGGAGAAITCAAACAG
 ACCTCGTCATTCTCTGGTGTGAGCCTGGTGGCTCACCGCCTATCATCTGCATTTGCCCTTACT
 CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
 TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
 ATCCTCCTTCATGCCCTCCCTCCCTTTCTACCCTGCTGAGTGGCCTGGAACTTGTTTAAA
 GTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
 TTCTAAGTAGACAGCAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
 TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTCTGGGCTCTTTCCTTGTTGACTGAC
 GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTG
 TGATGACACTGGGGTCTTCCATCTCTGGGGCCACTCTCTTCTGTCTTCCCATGGGAAGTG
 CCACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
 GGAAATGGGAGCTCTTGTTGTGGAGACATAGTAAATTTTCAGAGAAGTTGAAGCCAAAAG
 GATTTAAAACCGCTGCTCTAAAGAAAAGAAACTGGAGGCTGGGCGCAGTGGCTCACGCTG
 TAATCCCAGAGGCTGAGGAGGGCGGATCACCTGAGGTGCGGAGTTCGGGATCAGCCTGACCA
 ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
 CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 48

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYS GFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRV TFLPTGITFKSV TREDTGTYTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 49

CCCACGCGTCCGAACCTCTCCAGCG**ATG**GGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT
GCTTACAGTGTGCTATTCTCTGCTGTCAAACCTAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGCTGGAGAACAACATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCAGGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCAGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTCACG**TAGT**CTGGGAGGCAGGGGGCGAGCAGCCCCCTGGGCCGCTCCC
CACCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCGGAAGCATCCGAGCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAAGACAACCGTCTGGAGGTGGCTGTCTCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCTCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTGTTTGTGTTTCAGGAAAAAGAAAGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCTCACATTCCACGACCCAGGCCTGCACCCCAACCCCACTCCAGGCC
CGGAATAAAACCATTTTCTCTGC

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FIGURE 50

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFALKLIVETDTFGSRVRIKGAESEKYICMNRKGLIGKPSGKSKDCVFTEIVLENNYTAFQNAHEGWFMATFRQGRPRQASRSRQNRQEAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 51

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCTCAGGTGCATATT
GACAACCGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTACCCGTGAACATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCAGGTTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAGGCTGCCGCCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGAGGGGAACAAGAATACTTTGGGGGAAAAGAGTTTTAAAAAGAAATGAA
AATTGCCTTGAGATATTTAGGTACAATGGAGTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGAGCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAGAGCAAAA
AAAA

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FIGURE 52

MKTIQPKMHNSISWAIFTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNIRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTVRHHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPVVR RVKVTVNYPPISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGT SRRAGCVWLLPLLVLHLLKF

Signal peptide:

amino acids 1-28

[illegible]

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FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFOGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLDALSEGVGKAIGKEAGGA
 AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGQGNPGGGLTPWVHGYPGNSAGSFGM
 NPQGAIPWQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGGSGGSSNSGGGS
 GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSGSGSGSGSGSGSGSGSGSGSGSGSG
 GSSTGSSSGNHGSGGGGNGHKPGCEKPGNEARGSGESGIQGFRCQGVSSNMREISKEGNRLL
 GSGSDNYRGQGSWSGSGGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQ
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

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FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT
GGGGGTCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCTGCAAGTGTACAGCTTTGAGCACACCTACTTTGGCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACAGAC
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCTTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAATGATGTTAAAGTAAGAATTGCAAAA

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FIGURE 56

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHR
PSCTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

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FIGURE 57

GGAGCCGCCCTGGGTGTACAGGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCAGCCTCG
 GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTGCTGCGGTTTTTGTTCCTGGGGCTGA
 GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
 GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCAAGGGGAGGTGTCTTC
 ATCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
 AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
 ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTTA
 CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
 TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCTCGCGTCTCCAGGGGTGCCCCAT
 GTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
 GTGGGATCGGCAGCTTCCATCCTTCCAGACTTCTTTGCAACAGCATTAGATGTCATCCGTG
 GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGCTGCAAGGCCAC
 AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
 AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
 TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
 ATTGCTCCCGGACCCTGCCCTGGCCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
 TTCTCTGTACCTCCGCGACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
 TGACCCCCACGCCAGTCTCTCCAGCCAGGCCTGCCCTCACCAAGACTGCCACGACAGAT
 GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
 CATAGGTGCTGTGCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC
 CCCACCAC'TCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATATAAGGGTCACTCTAGCAC
 AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
 TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
 AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
 CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
 CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGCTCCCACTCCAGTCCCTGT
 ATTGATATAACCTGTCAGGCTGGCTTGGTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
 TTATTAACCAATACATGAAATATGTGTGTTTTCAATTTGCAAATTTAAATAAGATACATAA
 TGTTTGTATGAAAAA

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FIGURE 58

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
 SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
 SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
 WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
 VVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
 SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPISPIPGGVSSSGLSR
 MGAVPVMVPAQSQAAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

FIGURE 59

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTTTGTCTGTTATTTTTTTTTTCTTTTTCTTTTTCCACCACATTGTATTTTAT
 TTCCGTACTTCAGAAATGGGCCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTCTCT
 GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCAGAGTGTCACAAATCCTGGCCGTGCC
 CTAGTGTGTGCCGTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCGGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC
 TGGATTTCTCGCAGAAGTGCACAAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTTCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAAC
 AATATTACAGCCATTTACGGGGTGTCTTTGCCAGCTCTTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
 TCAATTTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCAATCCGACATGGCCCTCCAGAA
 TCTCAGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTTGACGTAATTTCGCTGTCC
 CACCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTCAGGACAAACAGAT
 AAACCACATTCCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGTGTACTCAAGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCTTGTGTTTTGTGACTGCAGATTAATAGGGTACAGAAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTTCATGTGCGAAGGTCCTGAACAAGTCCGGG
 GGATGGCGCTCAGGAATTAATATGAATCTTTTGTCTGTGCCACACGACCCCGGGCTG
 CCTCTCTTACCCCGAGCCCAAGTACAGCTTCTCCGACCCTCAGCCTCCACCCCTCTCTAT
 TCCAAACCTTAGCAGAAGCTACACGCCCTCAAACCTCTACCACATCGAAACTTCCACAGATT
 CTGACTGGGATGGCAGAGAAGAGTGACCCCACTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAAGTCAAGTGGCTCTCTCTCTTACCCTGATGGCATA
 CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTACAGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTAGAGCCCGGATCCACCTATCGGATT
 TGTTTAGTGCCATCTGAGTGCCTTTAACTACCGCGGTAGAAGACACCAATTTGTTACAGGC
 CACCAACCTTGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCATAGCAGACAGCA
 CGTCCACAGCATGGGCTCCCCCTTTTCTGCTGGCGGGCTTACGGGGCGCGGTGATATT
 GTGCTGGTGGTCTTGTCTCAGCGTCTTTTGTGTCATATGCACAAAAAGGGGCGCTACACCTC
 CCAGAGTGGAAAATACAACCGGGGCGGGCGGAAAGATGATTATTGGCAGGCGAGGCACCAAGA
 AGGACAACCTCCATCTCTGGAGATGACAGAAACAGTTTTCAGATCGTCTCCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTCAGACTGCAGCCCATTTACACCCCAATGGGGGCATTAATTA
 CACAGATGCCATATCCCCAACACATGCGATCTGCAACGACGCGTGCACAGCTGGAGC
 ACTGCCATACGTCAGCAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTTCTATTTCAAGTTAATTACAACAGTTTTGTAACCTTTGCTTTTTAAATCTT

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FIGURE 60

MGLQTTKWPSHGAFFLKSWLIIISGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFMNLKPNVRVLHLQENNIQT
 SRAALAQLLKLEELHLDNDSISTVGVEDGAFREAIKLLFLSKNHLSSVPVGLPVDLQELR
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPFPD
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
 PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMVRELNMMNLLSCPTTTPGLPLFTP
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVVL
 LSVFCWHMHKKGRYTSQKWKNRGRRKDDYCEAGTKKDNISILEMTETSFQIVSLNNDQLLKG
 DFRLQPIYTPNGGNYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 61

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGTCGCTTT
 TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAAACAAGA
 AAGTCAAGCAGCCAGTGGCATCTCATTGAGAGTGAAGCGCTGGCTGGGTGGAACCAATTT
 TTTGTACCAGAGGAAATGAATACGACTAGTCACATCGGCCAGCTAAGATCTGATTAGA
 CAATGGAACAATTTCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
 TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGTATAGAGAGGAGCGTACCTC
 TACATCTTAAGAGCCAGGTAAATAGACATCGCTACTGGAAGGGCTGTGGACCTGAGTCTGA
 GTTTGTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
 AGGCCATTGTACCAGAGATGTCCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
 GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
 ATATTTTCTGTTGAACCAACAACAGGAGTCAAGAATATCTTCTAAAATGGATAGAGAAC
 TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
 TCTGGAACAACAAGTGTATTAATTAACCTTTCCAGATGTTAATGACAAATAGCCCTATATTTAA
 AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
 TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTTGAAGAGCA
 GATTCGCAAAACATTGACATTATTACTAATCATGAAACTCAAGAAGGAATAGTTTATATTTAA
 AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAACCATC
 ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTTCATTAAAGTCCAG
 GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTCCATTTATGATTTTGAAGTTTTTGA
 AGAAAACCCCAAGGATTTATTTGAGGCGTGGTGTCTGCCACAGACCCAGACAAATAGGAAT
 CTCTATCAGGTATTCTATTCTAGGAGCAAGTGTTCATAGTGAATGATTAATGATCAATC
 ACTACAAGTAACCTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
 AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA
 ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGAANAATGCAGGCCTCT
 GGTCAAGTAAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAGAGACCAATTT
 TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTCACATCATAGATTAATCAAG
 ATAACACAGCTGTCTATTTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
 TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCCTTAC
 CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACTCGCCAGTACCAGGAGCTTG
 TGCTTTCCATGGGATTTCAAGACAGAAGTTATCATTTGCTATTTTCATTGTCATTATGATCA
 TTTGGGTTTATTTTGTACTTTTGGGTTTAAACACACGGAGAAAACAGATCTTATTTCCGTA
 GAAAAGTGAAGATTTTCAGAGAGAATATATTTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
 ATACAGAGGCCCTTGTATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGGAACGCAAGACT
 CGGAAAACCAAGCCGTGAGATCAGGAGCCTATACAGGCATGCTTTGCAAGTTGGCCGTCGA
 CAGTGCCATATTCAGGAATTTCAATCTGGAAAAGCTCGAAGAGCTAATACCTGATCCGTGTG
 CCCCCTCTTTGATTTCCCTCAGACCTACGCTTTTGAGGGAACAGGCTCATTAGCTTGGATCC
 CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
 GGGACCTCGCTTTAAAGATTAGCATGCATGTTTGGTTCTGCAAGTGCAGTCAAAATATAGG
 GCTTTTTACCATCAAAATTTTAAAGTGCTAATGTGATTTCGAACCCCAATGGTAGTCTTAA
 AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTC
 CTGGAGTAAATACTCCATGGTTATTTTAAAGTACCTACATGCTGTCTATTGAACAGAGATGTG
 GGGAGAAATGTAAACAATCAGCTCAGGCATCAATAACAACGATTTGAAGTAAATAATG
 TAGGAAGATATTAAGATGATGAGAGGACACAAGATGTAGTCATCCTTATGCGATTATAT
 CATATTACTTTAGGAAGAGTAAAAATACCAACAGGAAATTTAAAGGAGCAAAAATTTG
 CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
 ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATGTTTCTCTTAT
 TTAAT

amino acids 136-146 and 244-254

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FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCAATGGC
CGCCCTGCAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGAC
AAGTCCAACTTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACCTTACCCCTGAAGAAGTGCTGTTT
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCTTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTG
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTGACCAGAGCAAAGCTGAAAAATGAA
TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC
CAAAGGAAGATGGGAAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA
TAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTT
TTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTCCATTCCCTTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA
TAAGACTGCATTTTATTATATCATTTTATTAATATGGATTATTATATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

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FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185
><subunit 1 of 1, 179 aa, 1 stop
><MW: 20011, pI: 8.10, NX(S/T): 3
MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRFIGEKLFHGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:**Signal peptide:**

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 65

GCCCTAACCTTCCAGGGCTCAGCTCTTTGGAGCTGCCATTCTCCGGCTGCCGAAAGGA
 CGCGCGCCCTGCGTCGGGCGAAGAAAAAGCAAACTTGTCCGGAGGGTTTCGTCAATCAAC
 CTCCTTCCCGCAAACTTAACCTCCTGCCGGGGCCATCCTAGACAGAGGAAAGTTCTCTGCA
 GAGCCGACCCAGCCCTAGTGGATCTGGGGCAGGCAGCGGCGCTGGCTGTGAATTAGATCTGT
 TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCAACCGTCCCGGGCACC GGGTGG
 CGCTGCCCGAGTGGAAACGACAGTTTGCAGAGCTCGGCTGCAAGTGGCCCTCTCTCCCGCG
 GTTGTTGTTTCAGTGTCCGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCTCAGAGG
 TCCGAAGAGCGCTCGCTCCTACTCGCGTTCTCTCTCTCTCGGTTCCCTACTGTGA
 AATCGCAGCGACATTTACAAAGGCCCTCCGGGTCTACCGAGACCGATCCGCAGCGTTTGGCC
 CGGTGCTGCTATTGCATCGGGAGCCCCGAGCACCGGCGAAATGGCGAGGTTCCCGAAGGC
 CGACCTGGCCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTCACGGACCAAGTTTCAGTTTCG
 CCGATGGGAAACCCGGAGACCAAAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCT
 CACACAGAGGAGGAGGTGGAAAGTTGATTACACACCGGTACAGCCACAGGTGGAAAGAACTT
 GGACTTTCTCAAGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAAGACTCTCTGAGCCCA
 GAAGCTTCACAGACTGTGTCTGGATGATGGGCAGGACAATAACCACTCAGATCGAGGAGGAT
 ACAGACCAAAATTAATCATCTCAATATATGTTCCATGTATCTGCGAGCGGGGATTT
 ATGGGTGAACATAGACCAAAATGGAAAAAGATAAAGTGAAGATTTCATGGAATATTGTCCAATA
 CTCATCGGCAAGCTGCAAGAGTGAATCTGTCTTCGATTTTCCATTTTATGGCCACTTCTTA
 CGTGAATCACTGTGGCAACCGGGGTTTCATATACACTGGAGAAAGTCGTACATGGAATGCT
 AACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCAGTGTATCCAGAAAT
 CAACTGTAGATATTTTGATAAATGGCAGCACTTGTGGTCAGTGGGACCATGTACATCTC
 CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCTGCTCATGGATGGACGAAT
 CATCTTTGGATACAAAGAAATTCCTGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAG
 TGAAAGTCGGACTGTCGATGCATTTGTGCTTGCACAGGATCCAACAAATTCCAATGTT
 CGAAGAAGAACAAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTTACCAACAT
 TTCGGCTGTGGAGATGACCCCATTACCCACATGCCTCCAGTTTAAACAGATGTGGCCCTGTG
 TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAAACTTCAAAGATGTTCCAGTGGG
 TTTGATCGTCACTCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGT
 GTGTGAGAATACAGAACCACTGGAAACTTCTTCTCGAACCACCAAGCCGTGCGATGAAGTCA
 CCACCCAGTTTCAGGCTCCTAACTACCACCAGAAGAGCAGTGACTTCTCAGTTTCCACACGC
 CTCTTACAGAAGATGATACCAAGATAGCACTACATCTAAAGATGAATGGAGCTTACACAGA
 TGACAGTGCAGCTGAGAAGAAAGGGGAACCTCCACGCTGGCTCATCATTTGGAATCCTCA
 TCCTGGTCTCATTTGAGCCACAGCCATCTTGTGACAGTCTATATGTATCACCACCAACA
 TCAGCAGCCAGCATCTTCTTTATTGAGAGACGCCCAAGCAGTGGCTGCGATGAAGTTAG
 AAGAGGCTCTGGACATCCTGCCTATGCTGAAGTTGAACCAAGTTGGAGAGAAGAAGGCTTTA
 TTGTATCAGAGCAGTGCTAAATTTTAGACAGAACCAACCAACACACACAAACAGCTC
 TAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACACACACAAACAGCTC
 TAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCAGGAAACAAAGG
 TAAACAAAAAATAAACTTATACAAGATACCAATTTACACTGAACATAGAATCCCTAGTGG
 AATGTCATCTATAGTTCACTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA
 TAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAGGGATCAGAAAAAAAATCATAATAAGC
 TTTAGTTTCATAGGG

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FIGURE 66

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTAQFPHTEEVEVD SHAYS
 HRWKRNLDFLKAVDTNRASVGQDSPEPRSFDTLLDDGQDNNTQIEEDTDHNYYSRIYGPS
 DSASRDLWVNIDQMEKDVKI HGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTG
 EVVHRMLTATQYIAPLMANFDPVSRNSTVRYFDNGTALVVQWDHVLQDNYNLGSFTFQAT
 LLMDGRIIFGYKEIPVLVTQISSTNHVPKVGLSDAFVVVHRIQQIPNVRRTIYEHVELQ
 MSKITNISAVEMTLP LPTCLQFNRCGPCVSSQIGFNCSSWCSKLQRCSSGFDHRHQDWVDSGCP
 EESKEKMCENTEPVETSSRTTTTVGATTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLK
 DNGASTDDSAAEKKGTLHAGLIIGILVLIVATAILVTVMYHHPTSAAASIFFIERRPSR
 WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

FIGURE 67A

GCAGCCCTAGCAGGGATGACATGATGCTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTG
 GCTGGCGGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCTCCTGCCTCCCGGGTGGACAGA
 GTGTGGACTTCCCCTGGGCGGCGGTGGACAACATGATGGTCAGAAAAGGGACACGCGCGGTG
 CTTAGGTGTTATTTTGGAAAGTGGAGCTTCAAAGGGTGCTGGCTGAACCGGTCAAGTATTAT
 TTTTGGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
 GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGCCCATACAGCTGTTCT
 GTTCAGACTCAACATACACCCAGAACATGCAGGTGCATCTAACTGTGCAAGTTCCTCTCTAA
 GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGT
 TGGCCACTGGGAAACCAGAGCCTTCCATTCTTGGCGACACATCTCCCCATCAGCAAAAACCA
 TTTGAAAAATGGACAATATTTGGACATTTATGGAATTACAAGGGACACGGCTGGGGAAATATGA
 ATGCAGTGC GGAAAAATGATGTGTCTATTCCAGATGTGAGGAAAGTAAAGTTGTTGTCAACT
 TTGCTCCTACTATTAGGAATAATTAATCTGGCACCGTGACCCCCGGACGCAGTGGCCTGATA
 AGATGTGAAGGTGCAGGTGTGCGCCCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT
 CTTCAATGGCCAACAAGGAATATTATTCAAATTTTAGCAAGAATCCATTCTCACTGTTA
 CCAACGTGACACAGGACCTTCGGCAATTATACTTGTGTGGCTGCCAACAGCTAGGCCACA
 ACCAATGCGAGCCTCTTAAACCCTCAAGTACAGCCAGTATGGAATTACCGGGAGCGC
 TGATGTTCTTTTCTCTGCTGGTACCTTGTGTTGACACTGTCTCTTTTACCAGCATATTCT
 ACCTGAAGATGCCATTCTACAAATAATTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCT
 GAAAGTGTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAGACAGCGTGGGATATAATC
 AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAATACTTTTAAT
 TCTACTCTTTTGTATTGATACATTACCTTGTGAAGCATGATGGAATTACCGGGAGCGC
 ACGTGAAGGCTCTGAAATTAATTTAGAGGATATTAATGTGATTTCATGTTTGTAACTCTAC
 AACTTTTCAAAGCATTCAGTCAATGGTCTGCTAGGTTGACGGCTGTAGTTTACAAAAAGCAA
 TATTGCACTGAATATGTGATTCTTTAAGGCTGCAATAACAAGCATTCAGTCCCTGTTTCAAT
 AAGAGTCAATCCACATTTTCAAAGATGCATTTTCTCTTTTGTATAAAAAGCAATAATA
 TTGCCTTAGATTATTCTTCAAATAATAACACATATCTAGATTTTTCTGCTGCATGATAT
 TCAGGTTTCAGGAATGAGCCTTGTAAATAAATGAGTGTGACAGCTCTGCTTCTCTTCTCTGT
 AAGTTTCAGCATGGGTGTGCCCTTCATACAAATAATATTTTCTCTTGTGCTCCAACATATAAA
 AATGTTTGTCTAAATCTTCAAAATTGAAAGTAAAAATAAACAGAGTGATCAAGTTAAACCA
 TACACTATCTTAAGTAAACGAAGAGCTATTGGACTGAAAAATCTCTTCTGCACTGACAA
 TGGGTTTGAAGATTTCGCCCACTAAGTCTGTTGATGAGAGACAATTAATAAC
 AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA
 AATCATTTCCCTTTAAAAATGACAGCACAGTCCACTCAAAGGATTTGCTAGCAATACAGCATCT
 TTTCTTTCTAGTAGTCCAAGCAAAAAATTTAAGATGATTTGTGAGAAAGGCAACAAAGTCC
 TATCACTAATATTACAAGAGTTGGTAAGCGCTCATTAATTTTATTTTGTGGCAGCTTAA
 GTTAGTATGACAGAGGCAGTGTCTGCTGGACAGGACATTTTGCATATTTTCCATTTGAA
 GTACTCACTAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACTTCCAAAAATATATTA
 TAACAACATCTTATATCGGTATGTAGCAGACCAATCTCTAAAAATAGCTAATTTCTCAATAA
 AATCTTTCTATAGCCATTTCACTGCAACCAAGTAAAAATCAAAAAAGACCATCTTTATTT
 TTCTTTACATGATATATGAGATGCGATCAAATAAAGACAAAAACCCAGTGATGAGAATAT
 CTTAAGATAAGTAAATTAATTAATTTGTAATGTTAAATTTTCTACTATAAGAAAGCAA
 AACTCATATTTTGAAGGAAAAATGCTGTTACTTAAACATTAATTTACAGGAATAGTTTGAATG
 TTTCACTCTTTTACTAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGTATGAAGT
 ACCAATTTCACTAGTACCTAATTTCTACAAATAGTCCCTTTTACAGGTTGTAACAAAGTCC
 ACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATTATCTAG
 TATGTTGCCCTAGCAGGGATGGCTTAAAAACTGTGATTTTCTTTCAAGTAAAACTTAGT
 CCCAAAGTACATATAATCAATTTAATTAAGAAAAATGAATCTTAATGAGGGGACATAAG
 TATACTCTTTCCACAAAAATGGCAATAATAAGGCATAAAGCTAGTAATCTACTAAGTGAAT
 AAATGTATGACATATTTTGAATGATACATTAATAAAGAGTTTGTGAACAAATTTGGCAT
 TAACTTTATTTATTTTGTCTTTAAGAAATATCTTTTGTGGAATTGTTGAATAAATATAA
 AATATTATTTTGTATTCAGCTTTAAAGTGGCACACTCCATAATAATCTACTTACTAGAAAT

FIGURE 67B

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
 AAGAATGCATATTATTTCAGTGACCGCTTTCCTAGAGTTAAAAATACCTCCTCTTTGTAAGGTT
 TGTAGGTA AATTGAGGTATAAACTATGGATGAACCAATAATTAGTTCAAAGTGTGTCTATG
 ATTCCAAATTTGTGGAGTCTGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
 CAGTAGCTATATGTATTTGCCTTTATGTTAGAAGAGACTTCTTGAGTGACATTTTTAAATA
 GAGGAGGTATTCACATATGTTTTCTGTATCACAGCAGCATTCCTAGTCTTAGGCCCTCGGA
 CAGAGTGAAATCATGAGTATTTATGAGTTC AATATTGTCAAATAAGGCTACAGTATTTGCTT
 TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTTATGGACATATAA
 AATGTCTGATTACCCCATTTTTATCAGTCTGACTGTACAAGATTGTTGCAATTTTCAGAATAG
 CAGTTTTATAAATTGATTATCTTTTAACTATAACAATTTGTGTAGCTGTTTATTTCAGG
 ANTATATTTTCTACAAGTTCCTTGTGGGACTCCTTTTGTGCCCTATTTTTTTTTAAAG
 AAGGAAGAAAGAAAAATAAGTAGCAGTTAAAAATGAGAATGGAGAGAAAAAGAAAAAGAAATG
 AAAAGGAAAGGCAGTAAAGAGGGA AAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
 AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGGAAGGAAGAAATCAGAGTATTAGG
 GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAACATATGTTTTTCAA
 TGATCGCATTTGAAACATAAGTCCATATTATACCATTAAAGTTCCTATTATGCAGCAATTATAT
 AATAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGAGACACTAAAAGATTTGAG
 AGGGAGAATTTCAAAC TAAAGCCACTTTTGGGGGTTTATAACTTAACTGAAAAATTAATG
 CTTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGA ACTGAGAAAAATTACCCAG
 GTAATTCAGGGA AAAAAAAAAATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
 ACTCTGAAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAAATTG
 TTAATTTATCCATTGTGTCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
 AAAAAAATTGTTTTTGAATCCAGAAATGATTTAAAAAGAGTCAAGTTTTTAACTATTTA
 TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
 GATTCTTTGAAATATGTATTACTTTAAAGACTGGA AAAAGCTCTTCCTGTCTTTTAGTAAAA
 CATCCATATTTCTAACTGATGTA AATATGTTGTACTGTTCCAATAGGTGAATATAAAC
 TCA GTTTATCAATTA AA

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FIGURE 68

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259
><subunit 1 of 1, 354 aa, 1 stop
><MW: 38719, pI: 6.12, NX(S/T): 6
MDMMLLVQGACCSNQWLA AVL LSLCCLP SCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYL
EDGASKGAWLNRSSIIFAGGDKWSVDPRVSI STL NKR DYSLQIQNV DVTDDG PYTCSVQTQH
TPRTMQVHLTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQ
YLDIYGITRDQAGEYECSAENDVSFPDVRKVKVVNFAPTIQEIKSGTVTPGRSGLIRCEGA
GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASL
PLNPPSTAQYGITGSADVL FSCWYLVLTLSSFTSIFYLKNAILQ

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
304-310, 321-327**Myelin P0 protein.**

amino acids 94-123

ATAGTAGAAGAATGCTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTACATGGGCACA
ATTTTCACATTCAAGCTCCTTATCCTTAGGCTAATTTTATATTATGTTAAATCACTGTGTTTTTG
TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGC
AGCGCACATCGCTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT
TTAATTAAAGGGTTACATCCAACCCAGAGCGCTTTTGTGGCAGCTATGTTCTCCAGTCTCT
CGCTCACTGCGCGAGGAAGAGGGAAGAGTCCAGGCGTTAGACATGTATAGACAATAAAA
CAGCTGGAGATTGGGCTTAAAATACCCACCAAGCTCCAAAGAAGAGACCCAAAGTCCCCAAA
CATTGATTTTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA
GCCACAAGATGCCATTGTCCCCGGGCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC
CGTGGCCTGCCCTGAGGGTGGCCCCACCGGCCGAGACAGCAGCATATGCAGGAAGCGG
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCAG
GCCATGCGCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC
ACCCCTCCAGCAATCGCGCGCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCT
TCTCCTCTGCAAAT**TAG**

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FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175
><subunit 1 of 1, 155 aa, 1 stop
><MW: 17194, pI: 10.44, NX(S/T): 0
MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK
```

Important features of the protein:**Transmembrane domain:**

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

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FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATG**GC GTGGAGCCTTGGGA
 GCTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTC
 AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCCTTTTGCCAAAGG
 GAACCTGACTTTCACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATA
 CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC
 AGGGCTGAATTTGCAGATGAGCATTCAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGA
 CACCATTATTGGACCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTT
 TCTTAGCCCCATAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCA
 TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA
 GTATGACTTTGAGGTCCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAAGTTCGAG
 GGTTTCTTCCTGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAAACACC
 CATGACGAAACGGTCCCTCCTGGATGGTGGCCGTATCCTCATGGCCTCGGTCTTCATGGT
 CTGCTTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTAGC
 CCTTCTCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT
 AACACACTTCTGTTTTTCTCCTTTCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAG
 GTGCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA
 CCCCCTGGGCGAGGGGCCCAAGCT**TAG**GCCTCTGAGAAGGAAACACACTCGGCTGGGCACA
 GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAAACAAGGGCCAAGA
 CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT
 TTTAAAGGCTGTCTTTGGCAAAAATACTCCATTTTGGGAACCTCACTGCCTTATAAAGGCTTTCA
 TGATGTTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTTCAGCCTTTTATATCACTAAAATAA
 GATCATGTTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCACGCCGTGAATACCAGCA
 CCTTAGAGGTGCGAGGCAGGCGGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATA
 TGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTAT
 AATCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA
 GGTGCACTGAGCCGAGATAGCGGCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCAT
 CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACTTAAATGAGGAATAAGAATGG
 AGATGTTACATCTGGTAGATGTAACTTCTACCAGATTATGGATGGACTGATCTGAAAATCG
 ACCTCAACTCAAGGTTGGTCAGCTCAATGTACACAGAGCACGGACTTTTGGATTCTTTGCA
 GTACTTTGAATTTATTTTCTACCTATATATGTTTTATATGCTGCTGGTGTCCATTAAAGT
 TTTACTCTGTGTTGC

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FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSAALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTTECDFSSLSKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFOITPQYDFEVLRLNLEPWT
YCVQVRGFLPDRNKAGEWSEPVCETTHDETVPSSWMAVILMASVFMVCLALLGCFSLWCV
YKTKYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNP
DSCSLGTTPPGQGPQS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

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FIGURE 73

CGAGCGCCAACCCGCTAGCGCCTGAATCCGGCGTGCTGCCCGCTCGCCGCCCGCC**ATG**GGCCC
 GCGCAGCCCGCTGCTCGCCCGCTTGACCGCGCTCCTCGCCGCCCGCGCTGCTGGCGGAGAT
 GCCCGCGCGGGCAAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATTT
 TCTCCAGCAGCACTTTGGACCTCGGGTGCAGATCGACGTGTACGAGAAGGGAACCGTGGGTG
 GCCGCTTTGGCCACCATCTCAGTCAACAAGCAGCACATGAGAGCGGGGCTGCCTCCTTCCAC
 TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGCTGAGGCACCGGCGCGAGGT
 GGTGGGCAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC
 TGCTGAACCTCTTCCGCCCTCTGGTGGCACTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG
 GTGGAGGAGGTATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCACGGCTATGCCTT
 CTCGGGTGTGGAGGAGCTGCTCTACTCTACTGGGGGAGTCCACCTTTTGTTAACATGACCAGC
 ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCACGCAGCGCTTATTGATGATGTCTT
 TCTGCTGTCTTGGCGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCTTTGCAGGAGCCAT
 GTCCTAGCCGGGGCCCAAGCGAGCCCTGTGGTCTGTGGAAAGGAGGCAATAAGCTGGTTGT
 CCGGTTTGTGTAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTGACCTCTGTGACCTG
 CACAGCACAGAGGGGAAAGCCCTGTACCAAGGTGGCGTATGAGAATGAGGTAGGCACAGCTC
 TGACTTCTATGACATCGTGGTCAATCGCCACCCCTGACACTGGACAGCAGCAGGCAACT
 TAACCTTTGAGGCTTCCACCCGCCCATTTGATGACGTGCAAGGGCTCTTCCAGCCACCGCT
 GTCTCCTTTGGTCCACGGCTACCTCAACTCGTCTACTTCGGTTTCCCAAGCTTAAGCTTTT
 CCCCTTTGCCAACATCCTTACCACAGATTTCACAGCTTCTTCTGCACTCTGGACAACATCT
 GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCAAGGAGGCACTGTTGGCGA
 GTCAGTCCCCCAAGCCCTCTTTCCGAGCCAGCTAAAGACCTGTTCGTTCTCTATTACTC
 AGTGACAGACAGCTGAGTGGCAGGCCCATCCCTCTATGGCTCCCGCCCCAGCTCCCGAGGT
 TTGCACTCCATGACCACCTCTTCTACCTCAATCGCTGAGTGGGCGGCCAGCTCCGTGGAG
 GTGATGGCCGTGGCTGCCAAGAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT
 AGACAAGATTGATCAAAAAGATTGTATGCACAAGGTCAAGACTGAACGTGTGAGGGCTCTAGG
 GAGAGCCTGGGAACTTTATCCCCCACTGAAGATGGATCATCCCAAGCAGCCAGGACTGA
 ATAAGCCATGCTCGCCCAACAGGCTTCTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG
 ACCTACTGTCTGCCTATATTAAGGCTCCACACGGCGCTGTGCTTTTTTTAAGGGGAAA
 GTAAGAAAAGAGAAGGAATCCAGCCAGTATATTTGTTTATTTATTTTAAAGAAGAA
 AAAAGTTTATCTTTCACAAGGTGCTTCAGACTTGGTTTCTTAGCTAGAAACCAGAAGACTACG
 GGAGGGAATATAAGGCAGAGAACTATGAGTCTTATTTTATTTACTGTTTTTCACTTACCTCA
 CCACATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAAACAGATGGTTACAAA
 TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCCTGGTTACTGTGGACT
 TGATGGATTGAAGTACCTAGTTTCAGAACTCCCTAGTCACCATCCAGCCCTGTCAACATC
 ACTGCATATTGGAGGAGATGACTGTGGTAGGACCAAGGAAGAGATGTGTGCCTGAATAGTC
 GTCACCATATCTCCAAGCTTCTTGGCAACCACTGGGAAAAGAAACATGCCAGGCTGTAGGAA
 GAGGGAAGCTCTTCTTGGCACCTAGAGGAATTAGCCATTCTTCTCTTATGCAAGATTGA
 GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGGTAGAGAGCAGTCATATCTTACCCC
 TAGATGTTTCATCCAGCAGAAGAAAGAAAGAGTGTGGGTAGGATCTTCAGAGGTTAGC
 CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTT
 TTCTACAAACCCTTAAAAATCACTTGTTTTAAAGAAAGTAAAGGCCCTTTTCATTCAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510
><subunit 1 of 1, 494 aa, 1 stop
><MW: 54646, pI: 7.27, NX(S/T): 6
MARAAPLLAALTALLAAAAAGGDAPPGKIAVVGAGIGGSAVAHFLLQQHFGPRVQIDVYEKGT
VGGRLATISVKNQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGSAIFGGEHFMLEETD
WYLLNLFRLWWHYGISFLRLQMWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTQRFIDDVSAVLRASYGQSAAMPAFAGAMSLAGAQQSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVSLVHGYNSSYFGFDPKLPFPANILTTDFPSFFCTLD
NICPVNISASFRRKQPQEAAVWRVQSPKPLFRTQLKTLFRSYYSVQTAEQAHPLYGSRPTL
PRFALHDQLFYLNLEWAASSVEVMAVAAKNVALLAYNRWYQDLKDIDQKDLMHKVKTEL

Important features of the protein:**Signal peptide:**

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
237-243, 429-435